

BIOLOGY AND MEDICINE



Diver Phil Forte vacuums the sea floor of McMurdo Sound for samples of foraminifera, a single-celled creature. Typically, "forams," as they are called, carpet deep-sea floors, but they also emerge in the shallow waters of Antarctica, making them available for study. (NSF/USAP photo by Steve Alexander)

Antarctica is a place like no other; as an intriguing habitat, it is a scientist's dream. It is a land where water is scarce-truly a desert-despite having more than two-thirds of the world's freshwater supply trapped in ice. Though it borders the world's major oceans, the Southern Ocean system is unique in the world, a sea where average temperatures do not reach 2°C in summer, where even the water is so unique that it can be identified thousands of kilometers away in currents that originated here. As the Earth, tilted on its rotational axis, makes its elliptical journey around the Sun each year, the Sun "sets" in April, not to be seen again until September. And the ice-an unimaginable, incomparable vastness of ice-appears in a dozen different varieties, at times and in places several thousand meters thick; there are two major ice sheets that change dynamically all the time. (The eastern sheet is larger than most countries.)

Adaptations and behavior developed in response to these extreme conditions provide insight into the intricacies, as well as the fundamental processes, of evolution. These extremes have also driven the development of ecosystems simple enough to reveal wonderfully clear pieces of the web of life on Earth.

The Biology and Medicine program funds research to improve understanding of antarctic ecosystems and life forms-their physiology, genetics, behavior, adaptations, and relationships. Projects range across all organizational levels, from the molecule, gene, cell, and organism to relationships within communities and ecosystems, to the level of global processes and the biosphere. This is another area of inquiry where scientific goals and benefits extend far beyond learning (in this field, about flora and fauna) in the high latitudes. Support is focused on the following areas:

- **Marine ecosystem dynamics:** Among the research topics are understanding the natural variability of marine ecosystems, correlating the structure and function of the marginal ice-zone ecosystem with oceanic and atmospheric processes, exploring the sources of nutrition and their influence on prey and on primary production, and the role of marine phytoplankton in carbon-dioxide cycling.
- **Terrestrial and limnetic ecosystems:** Organisms in ice-free areas and in perennially ice-covered lakes

show remarkable adaptations to extreme environments. Relatively few species thrive here, which facilitates the study of ecosystem dynamics and the interpretation of experiments, although much more remains to be learned about adaptive mechanisms and evolutionary processes.

- **Population biology and physiological ecology:** At the next level, looking at relationships among organisms, studies have focused on the variability and dynamics of populations of krill and other zooplankton. Ecological relationships among and between fish species, marine mammals, and birds have also been the object of much research, with many issues still to be further explored. Advances in genetic testing now permit scientists to establish relationships that were previously unverifiable between individuals and species in the wild. As organized programs of antarctic science enter their fifth decade (some have been in existence even longer), data sets and ongoing observations are elucidating manmade as well as natural changes.
- **Adaptation:** Antarctic extremes present a fundamental research opportunity; topics include low-temperature photosynthesis and respiration; enzymatic adaptations, and adaptive physiology, such as the development in fish of antifreeze compounds and modifications to the circulatory system in seals. There is also continuing interest in the response of organisms to increased ultraviolet-B radiation from the ozone hole (as well as its impact on them). Here, too, new molecular DNA advances have had a profound impact on the types of studies that can be mounted.
- **Human behavior and medical research:** Antarctica's extreme climate and terrain impose a quite spartan and unconventional existence on scientists and others who live and work there. As people are subjected to social, psychological, and physiological stresses (exacerbated during the winter isolation), opportunities for research arise. Studies focus on epidemiology, thermal regulation, immune system function, individual behavior, and group dynamics.

Function and chemical nature of ice-active substances associated with sea-ice diatoms.

James Raymond, University of Nevada-Las Vegas.

Sea-ice diatoms (a class of algae) are plentiful in the ice platelet layer and congelation ice in McMurdo Sound. Previous work suggests that these diatoms produce extracellular ice-active substances (IASs), molecules with large molecular weights that appear to be glycoproteins. The IASs seem to be associated with each species of sea-ice diatom. Because similar molecules have not been found in temperate-water diatoms, they apparently have a function related to cold or icy environments.

The IASs represent a novel type of ice-binding molecule that is distinct from the antifreeze proteins and glycoproteins found in some fish species. The IASs also do not lower the freezing point as fish antifreezes do, so their function is unclear. One possibility is that they help preserve cells when they are in the frozen state, so that when they thaw, a higher percentage will survive.

We will examine several questions about the function and chemical nature of these unusual molecules:

- The IASs appear to have cryoprotective properties. To explore this possibility, we will assess the IASs' ability to prevent freeze-thaw damage in whole cells. Survival will be assayed by uptake of carbon-14-labeled bicarbonate. We will also investigate the ability of the IASs to inhibit the recrystallization of ice, which is a common measure of antifreeze activity in plant studies.
- The IASs are known to bind to ice crystals. To better understand the mechanism involved, we will conduct additional studies to determine the specific crystal faces to which they bind.

- We will try to better characterize the chemical nature of the carbohydrate and protein components found in the IASs by means of mass spectrometry, amino acid sequencing, and other techniques.
- We will attempt to raise antibodies against the IASs, since these will have several uses in determining the origin, seasonality, relatedness, and possibly the function of these molecules.
- We will attempt to harvest sea ice from the Polar Sea as a new method for obtaining IASs. (BO-001-M; NSF/OPP 00-88000)

Antifreeze protein in antarctic fishes: Ecological and organismal physiology, structure-function, genetics, and evolution.

Arthur DeVries, and Chi-Hing Cheng, University of Illinois.

Despite temperatures that can dip below 0°C, antarctic waters provide a life-sustaining environment for a number of fish species. How are they able to take the most frigid waters on Earth through their gills without freezing? A primary reason is the so-called antifreeze proteins, an adaptation found in a number of polar and subpolar species. These biological molecules have an effect similar to that of antifreeze in a mechanical engine. The Southern Ocean provides the ideal laboratory and molecular biology the ideal probe to study this phenomenon. As the world's coldest marine environment, the near-shore waters of Antarctica, replete with ice crystals, hover just above the freezing point of sea water.

We are studying the physiology of fish and larvae from these waters to see how ice grows in biological tissues—a crystallization process called nucleation—and how antifreeze glycoproteins inhibit it. Evolving the antifreeze function has enabled antarctic notothenioids to colonize their frigid habitats very successfully. We are mounting comprehensive multidisciplinary analyses of this adaptation at the level of the gene as well as the protein.

Specifically, we will

- examine the structure of antifreeze proteins,
- refine the molecular model of how these proteins adsorb ice and inhibit the growth of ice crystals,
- study the physiological parameters governing the natural growth of ice crystals,
- pinpoint the chromosomal locus of the gene family and its protease progenitor gene,
- sketch its evolutionary history by calibrating the rate of notothenioid nuclear protein coding sequences, and
- focus on when these antifreeze glycoproteins develop during embryogenesis and early larval stages. (BO-005-M; NSF/OPP 99-09841)

Energetics of protein metabolism during development of antarctic echinoderms.

Donal T. Manahan and Robert Maxson, University of Southern California.

Larval forms are dominant in the life history strategies of invertebrates in marine environments. In Antarctica, energy budget calculations have shown that larval stages of echinoderms (radially symmetric marine animals like starfish and sea urchins) have the capacity to survive for years without food. This has led to the speculation that

mechanisms of energy metabolism are more efficient in these larval forms and that this enhanced efficiency might be unique to life in extreme cold.

Embryos and larvae of an antarctic sea urchin have high rates of protein synthesis while maintaining low rates of metabolism. The cost of protein synthesis in this antarctic sea urchin is 1/25th that reported for other animals. This is the lowest cost (highest efficiency) for protein synthesis ever reported and has important implications for the physiology of animal growth and development in cold environments. We intend to investigate this unique biochemical efficiency in detail.

Our experimental plan has three major objectives:

- to test the generality of the low cost of protein synthesis in antarctic sea urchin larvae by measuring metabolism and protein synthesis during development of other antarctic echinoderm species,
- to directly test the hypothesis that a high rate of protein synthesis with low metabolic cost means that growth efficiencies will be high in such organisms,
- to explain in specific molecular terms the unique high efficiency of protein synthesis in antarctic sea urchin embryos by studying each of the component processes of protein synthesis.

We will also supplement these measurements with measurements based on selected individual proteins. At the subcellular level, rates of ATP consumption during protein synthesis will be measured in cell-free translation systems of sea urchin embryos. The combination of these quantitative analyses will enable us to pinpoint those aspects of protein metabolism that result in such extremely high-energy efficiencies.

Understanding metabolic efficiency in polar organisms will help resolve questions about temperature compensation and adaptations to food limitation in polar regions. Our approach will emphasize the cellular and subcellular levels of biological analysis in order to understand the relationship between development, growth, metabolic rate, and rates and costs of protein synthesis in these organisms. We will test the hypothesis that there is a "new" biochemistry for protein synthesis in these organisms. (BO-006-O; NSF/OPP 01-30398)

Use of long-term database and molecular genetic techniques to examine the behavioral ecology and dynamics of the Weddell seal (*Leptonychotes weddellii*) population.

Robert A. Garrott and Jay Rotella, Montana State University-Bozeman, and Donald Siniff, University of Minnesota.

The study of the Erebus Bay Weddell seal population in eastern McMurdo Sound was initiated in 1968 and represents one of the longest intensive field investigations of a long-lived mammal in existence. Some 15,636 animals have been tagged, with 144,927 resighting records in the database.

We intend to build on this foundation with two lines of investigation that combine the long-term database with new field initiatives. We will maintain the continuity of the demographic data by annually marking all pups born, replace lost or broken tags, and perform multiple mark-recapture censuses. The new data will be combined with the existing database, and a complex series of demographic analyses will be performed. These analyses will allow us to test hypotheses about population regulation, as well as temporal and spatial patterns of variation in vital rates among colonies within the population.

A sample of adult female seals and pups will be weighed, and body morphometrics will be obtained using digital photography combined with image analysis software. Regression equations will be developed from these data to predict body mass. At each major colony within Erebus Bay, these regression equations will be used to estimate annually the parturition and weaning mass of a large sample of adult female seals and their associated pups. We

will also employ satellite imagery to track sea-ice extent in McMurdo Sound. The extent of sea ice affects regional primary productivity, which may increase marine resources, thereby having a positive effect on foraging efficiency and leading to increased body mass. These data, combined with the large proportion of known-aged seals in the current study population (more than 60%), will allow us to develop a powerful database to test specific hypotheses.

Learning about the mechanisms that limit and/or regulate Weddell seal populations and the specific biophysical links between climate, oceans, ice, and antarctic food webs can make an important contribution toward understanding pinniped population dynamics, as well as add to the understanding of population, community, and ecosystem patterns and processes. Continuation of this long-term study may also contribute toward understanding the possible detrimental impacts of human activities such as global climate warming and the commercial exploitation of antarctic marine resources. And, finally, the study can contribute significantly to the development and testing of new research and analytical methodologies that will almost certainly have other applications. (BO-009-M; NSF/OPP 97-25820)

Community dynamics in a polar ecosystem: Benthic recovery from a large-scale organic enrichment in the Antarctic.

Stacey Kim, San Jose State University.

In 2002-2003, McMurdo Station, the U.S. research station that houses over 1,100 people during the summer season, is completing construction of a sewage treatment plant that will be online in 2003. The existing outfall is a large source of organic enrichment (135,150 liters per day of untreated sewage); the new plant will output a small fraction of this amount.

The organically enriched outfall area and surrounding unperturbed areas have been well described. Detailed community descriptions of the epi- and infaunal community at the outfall location before effluent release are available and were collected over a long period (1988 to 1998), which minimizes the interannual variability.

We will examine community responses in a polar soft-bottom subtidal system to test the generality of an already elucidated paradigm. Community recovery rates from iceberg scours and anchor ice have been described. We hypothesize that recovery rates following cessation of organic input will be on the same scale as benthic community recovery from seasonal ice-mediated disturbances and as recovery rates in temperate systems. We will build on a 10-year time series that follows benthic community degradation resulting from a sewage outfall. Sampling will span the implementation of sewage treatment. To test the generality of recovery patterns, the data will be incorporated in a meta-analysis of community recovery from organic disturbance in a variety of habitats. Experimental manipulations will compare the roles of burial and patch size. In addition, efforts will be directed at microbial biochemical response and diversity, in tandem with the recovery of the infaunal community.

The knowledge gained from this research can be applied to any high-organic loading in polar habitats. Significant anthropogenic inputs in high latitudes include pulp mills and increases in human occupation and visitation (gray water dumping from boats). Natural sources, including woody debris in river outputs and carcass-falls from the productive surface waters above, also present significant carbon input. In the McMurdo area, marine mammals and large fish are abundant and add fecal material to the system. Supply vessels dock in Winter Quarter's Bay, and the number of tourist cruises is increasing. By using an integrated approach to evaluate the recovery of the microbial, infaunal, and epifaunal assemblages after a massive, 10-year carbon-loading perturbation, this study will further the understanding of anthropogenic impacts in polar environments. (BO-010-O; NSF/OPP 01-26319)

Hunting behavior and energetics of free-ranging Weddell seals.

Randall Davis and Markus Horning, Texas A&M.

Weddell seals (*Leptonychotes weddellii*) are the apex predators in the antarctic marine ecosystem, in large part because of behavioral and energetic adaptations that enable them to forage in the cold, dark, fast-ice environment. Earlier work pioneered the use of an animal-borne video system/data logger to record the behavior,

physiology, and locomotor performance of marine mammals at depth. For the first time, we witnessed seal hunting strategies and predator-prey interactions and were able to make corresponding estimates of diving metabolism. Here we follow up on those results and hope to provide insight into the foraging tactics of marine mammals and contribute to the fields of physiology (diving and energetics) and ecology (foraging theory and behavioral ecology).

By using isolated ice holes, we formerly preserved the seals' ability to choose the depth and duration of a dive, but left them no alternative but to return to a single place to breathe, thus limiting their range. We did not permit them to haul out of the water or interact with other seals on the ice, and thus they may have been exposed to fewer prey than when foraging naturally. Now we want to remove those constraints and focus on the behavior and energetics of completely free-ranging seals. Although the "constrained" study demonstrated important new principles in Weddell seal foraging and has increased our understanding of diving behavior and swimming performance, we believe that it is now essential to determine whether those principles apply to unconstrained animals.

To answer this question, we will test hypotheses related to the general foraging strategy, foraging location, searching mode, detection of prey, locomotor performance, cost of diving, and foraging efficiency of free-ranging Weddell seals. In addition, we will examine locomotor performance and behavior during diving to estimate the costs associated with hunting and the benefits gained from it (the type and frequency of prey captures).

The study will continue to employ a multidisciplinary team of scientists with highly skilled technical support. The results will advance our understanding of the foraging ecology of Weddell seals and create a basis for similar research on other species of marine mammals that are more difficult to study in the open ocean. (BO-017-O; NSF/OPP 99-09422)

Ontogeny of aerobic capacity, lipid metabolism, and elevated myoglobin concentrations in the skeletal muscles of the Weddell seal (*Leptonychotes weddellii*).

Shane B. Kanatous, University of Texas, and Rhonda Bassel-Duby, University of Texas Southwest Medical Center.

What is the temporal development of aerobic capacity, lipid metabolism, and oxygen stores in the skeletal muscles of young Weddell seals, and which aspects of the cellular environment are important in the genetic regulation of myoglobin expression during maturation? We will address this broad question during a 2-year study that will collaborate with an ongoing study of the diving and hunting behavior of free-ranging adult and subadult Weddell seals (see project BO-017-O). Results from our previous collaboration characterized the enzymatic, ultrastructural, and vascular adaptations for diving that occur in the skeletal muscles of adult Weddell seals. This study builds on those results to investigate the ontogeny of these adaptations and the genetic control of their development.

Our first objective is to characterize the ontogenetic changes in aerobic capacity, lipid metabolism, fiber type, and myoglobin concentration and distribution using enzymatic, immunohistochemical, and myoglobin assays in newborn, newly weaned, subadult, and adult seals. Our second objective is to determine the molecular controls for changes in the concentration and distribution of myoglobin in skeletal muscles during maturation. Through subtractive hybridization and subsequent analysis, we will determine the differences in mRNA populations in the swimming muscles of the different age classes of Weddell seals. These techniques will allow us to identify the proteins and transcription factors that influence ontogenetic changes in myoglobin concentration. The results will increase our understanding of both the ontogeny and molecular mechanisms by which young seals acquire the physiological adaptations they need to become competent divers and marine predators.

In addition, this study will advance our knowledge of the molecular regulation of myoglobin in skeletal muscle, which has broader applications for human medicine. Our collaboration with research on the diving and hunting behavior of Weddell seals will enhance the results of both studies, minimize the number of adult animals handled, share personnel, and reduce the need for additional logistical support. (BO-018-O; NSF/OPP 01-25475)

Yeasts in the antarctic dry valleys: Biological role, distribution, and evolution.

Laurie B. Connell, University of Maine; and Russell Rodriguez, University of Washington.

The soil community of the antarctic polar desert comprises few endemic species of bacteria, fungi, and invertebrates. Both filamentous and single-cell fungi have been isolated from a diversity of antarctic soil types, but only yeasts appear to be endemic to the polar desert soils. Although their ecological role in antarctic soils is undefined, yeasts may be the principal taxa synthesizing the sterols required by soil invertebrates. In addition, yeasts may be involved in accumulating and mobilizing growth-limiting nutrients such as phosphorus into the polar desert food web. Although yeasts have been well described in agricultural and industrial systems, little is known about their ecological role.

This multidisciplinary, collaborative research will characterize the role(s) soil yeasts play in the McMurdo Dry Valley ecosystem in order to better understand polar deserts and other extreme environments, as well as provide a foundation for incorporating yeasts into biogeochemical models of temperate environments. Soil microbiota mediate most processes such as decomposition, soil respiration, uptake and fixation of micro- and macronutrients, and detoxification of heavy metals and serve as major global carbon sinks. The complexity of soil communities in temperate regions poses difficulties in studying the relationships between biotic and abiotic parameters, and the factors controlling populations of soil microbiota remain poorly understood. The extreme climate and relatively simple community structure of the continental antarctic desert lend themselves to such studies.

We will first correlate the abundance and distribution of yeasts in polar desert soils with physical and chemical soil properties. Several physiological parameters will be explored in vitro to develop a basis for understanding the functional role(s) these organisms might have. Sterols synthesized by McMurdo Dry Valley soil yeasts, as well as their ability to survive multiple freeze-thaw cycles, will be characterized. The capacity of indigenous antarctic yeasts to use, compete for, and store phosphorus will be ascertained. The evolution of dry valley yeasts will be addressed by determining intra- and intervalley relatedness patterns based on DNA sequence.

Both soil samples and extracted DNA will be shared with other interested laboratories. Moreover, students from middle school (Biolab Inc.) through college (University of Maine) will be given the opportunity to collaborate on this project, as well as to develop their own projects. (BO-019-O; NSF/OPP 01-25611)

Participation in the Italian Ross Sea expedition.

Diane K. Stoecker, University of Maryland.

This project is an outgrowth of previous collaboration between Horn Point Laboratory, University of Maryland Center for Environmental Science, and the University of Trieste and the Laboratory for Marine Biology, Trieste, Italy. In December 2002, we will sail from New Zealand as part of the Italian expedition to the Ross Sea and land at the Italian station at Terra Nova in early February 2003.

Previous collaboration has involved the grazing dynamics and physiology of plankton from temperate coastal systems in the Adriatic Sea and the Chesapeake Bay. Techniques that have been recently developed to investigate the autecology (the ecology of individual organisms or individual species) and population dynamics of temperate, coastal, bloom-forming algae will be applied to polar protists from the Ross Sea. We will compare the role of microzooplankton grazing in bloom dynamics in temperate and polar systems, determine whether polar microplankton have ectocellular protease activity, and obtain samples of the photosynthetic ciliate, *Mesodinium rubrum*, and its algal "prey" from the Ross Sea for molecular analysis.

Microzooplankton (primarily dinoflagellate and ciliate) grazing is important in regulating the growth of many bloom-forming phytoplankton in temperate estuaries. We know that blooms can initiate only during windows of opportunity when grazing pressure by microzooplankton is low, but little is known about the specific grazing of microzooplankton on bloom species in polar seas.

We also intend to determine whether polar phytoplankton have cell surface enzymes that could be involved in the use of dissolved organics. Temperate dinoflagellates have considerable leucine amino peptidase activity and thus may be able to use polypeptides and proteins as a source of carbon or nitrogen. The research undertaken on this collaborative cruise will advance comparative studies of temperate and polar marine ecosystems and the physiological ecology of temperate and polar protists. (BO-020-E; NSF/OPP 02-30775)

Collaborative research: The chemical ecology of shallow-water marine macroalgae and invertebrates on the Antarctic Peninsula.

Charles D. Amsler and James B. McClintock, University of Alabama-Birmingham, and Bill J. Baker, University of South Florida

Many organisms are not mobile and so cannot escape from predators. One way they can keep from being eaten is to make themselves unappetizing by producing defensive chemicals known as secondary metabolites. However, the energy and other resources that go into making these compounds could instead have gone into growth or reproduction. We are studying the evolution of these tradeoffs and hope to understand ways that organisms maximize the usefulness of their investments in defensive chemistry.

For marine plants, the physical environment of Antarctica is very different from most other places in the world's oceans because nutrients are plentiful but light is often limited. So the "currency" that is used to "pay" for defense, growth, and reproduction is different than for plants in most other marine communities. This allows us to test theories about the costs and benefits of defense in ways not possible elsewhere in the world.

For marine animals, Antarctica is unique in that predation by sea stars is much more important than in other marine communities. Sea stars feed by extending their stomachs from their mouths and digesting prey outside their bodies. We predict that this should lead to a much higher investment in defensive metabolites in the outer layers of the prey. One of the main goals for our 2002-2003 season will be to test the hypothesis that sponges (an important component of these communities) will maximize their investment in chemical defense by having the highest levels of defensive secondary metabolites in their outermost layers.

This research should also advance our general understanding of the evolution of chemical defenses. We hope to elucidate the nature and role of bioactive agents in the specific ecology of the antarctic marine benthos (that is, organisms living at the bottom of marine environments). (BO-022-O; NSF/OPP 01-25181 and NSF/OPP 01-25152)

Food-web structure across a large-scale ocean productivity gradient: Top predator assemblages in the southern Indian Ocean.

George L. Hunt, University of California-Irvine.

During an Océan Indien Service d'Observation cruise, we will test the hypothesis that the dispersion and community of top predators vary with large-scale differences in physical structure and ocean productivity by conducting an interdisciplinary survey of marine bird and mammal use of distinct domains in the southern Indian Ocean. Our French colleagues will sample physical characteristics of the ocean and ocean productivity while we survey top predator distributions across a 35° latitudinal gradient from subtropical to subantarctic waters.

We will address the primary hypothesis that top predator assemblages are structured by spatial gradients in hydrographic properties and ocean productivity patterns known to influence the distribution and patchiness of their zooplankton, fish, and squid prey. We hypothesize that the overall abundance of marine top predators within a specific domain is largely determined by ocean productivity. Further, we hypothesize that the energetic costs of foraging determine which types of marine top predators inhabit specific domains. Species with high foraging costs must exploit dense prey aggregations within highly productive areas. Conversely, taxa with low foraging costs are able to inhabit areas of low productivity, where they exploit more dispersed prey.

To test these hypotheses, we will quantify the spatial association of top predator assemblages with specific water masses and the aggregate response of top predators at hydrographic and bathymetric domains. Because top predators respond to oceanographic variability at multiple scales of time and space, we will assess their responses to habitat variability at two specific scales. At the mega-macro scale [thousands of kilometers (km)], we will characterize faunal associations with specific water masses and ocean productivity domains. At the coarse scale (tens of km), we will quantify top predator aggregations at frontal systems and continental shelf margins.

We will employ a variety of analytical methods, including compositional analysis of coarse-scale habitat preferences, generalized additive models, recurrent group analysis, ordination of hydrographic data and top predator assemblages, and measurement of top predator aggregation using Lloyd's index of dispersion and autocorrelation statistics.

More specifically, we will study how overall top predator abundance and the distributions of distinct assemblages and feeding guilds change across spatial gradients in physical and biological properties. This interdisciplinary perspective will enhance our understanding of the way physical and biological processes structure pelagic communities in the southern Indian Ocean. (BO-025-O; NSF/OPP 02-34570)

Cultural emergence and health in Antarctica.

Timothy Dye, and Nancy Chin, University of Rochester.

The emergence of a long-term population in space will, in many ways, parallel the emergence of a sustained population in Antarctica, where development has expanded beyond the initial population of scientific and military personnel and now includes support staff and construction personnel. Experts speculate that a similar mix of residents may emerge as space populations develop. Such organizational and cultural merging in restricted environments undoubtedly creates new cultural landscapes (ethnoscapes) that could influence health and health behavior. Because of the extreme environmental circumstances, health risks and health care are particularly important. The study of cultural emergence in Antarctica as an analog to space could prove useful in the development of models of health and health behavior in an isolated confined environment (ICE) and could help planners better structure these environments to reduce health risks and identify factors that predispose people to those risks.

We aim to

- model the emergence of cultural stages in ICE ethnoscapes as experienced by both short- and long-term populations;
- identify those elements of ICE ethnoscapes that are specific to an individual season and those that are repeated;
- relate how the temporal and content stages of ICE ethnoscapes interact with risk, behavior, and injury; and
- demonstrate the utility of electronic and distance-based assisted ethnography in the conduct of social research in ICE environments of Antarctica, and possibly in space.

We will begin with key informant interviews and focus groups conducted throughout the United States with people who have spent at least one season on the ice within the past 3 years. The purpose is to elucidate the behaviors, risks, and health events that face residents, particularly in the emergence of ethnoscapes. The next phase has us residing in Antarctica for an extended period and conducting onsite participant observation and interviews at two different sites. This phase will include the Self-Disclosure Technique (SDT), an anthropological

method for identifying the conceptual structure of a cultural event. SDT will be used to describe cultural dynamics in occupational, recreational, spiritual, and other group activities. Fieldwork will involve both short- and long-term residence. The data will be processed, and models will be tested for validity with informants on the ice.

This research could contribute to the development of screening procedures for long-term residence in ICEs and context-sensitive explanatory models of culture and injury risk, as well as illustrate the utility of distance-based ethnography. (BO-027-O; NSF/OPP 01-25893)

Geographic structure of Adélie penguin (*Pygoscelis adeliae*) populations: Demography of population expansion.

David G. Ainley, H.T. Harvey and Associates; Nadav Nur and Grant Ballard, Point Reyes Bird Observatory; and Katie Dugger, Southern Illinois University.

We are investigating the mechanisms responsible for the geographic structuring, the founding of new colonies, and the recent population expansion of the Adélie penguins of Ross and Beaufort Islands. Similar expansion has been occurring throughout the Ross Sea, where 30 percent of the world population of this species resides, and is in some way related to ameliorating climate. Thus far we have been examining

- the relative importance of resources that constrain colony growth (the amount of nesting habitat versus access to food);
- aspects of natural history that might be affected by exploitative or interference competition among neighboring colonies (breeding success and foraging effort);
- climatic factors that influence the latter, especially extent and concentration of sea ice; and
- behavioral mechanisms that influence colony growth as a function of initial size and location, emigration, and immigration.

None of the colonies is nesting space limited, and we have shown how sea-ice extent and concentration affect diet, foraging effort, and winter survival. In addition, large colonies affect the foraging patterns of smaller ones within range and, perhaps, ultimately their size. The rate and direction of emigration also appear to be constrained by sea-ice conditions, with reasonable concentrations of ice favoring growth of smaller colonies where foraging competition is minimal. Yet to be determined is the demographic mechanism of colony growth (or decline). Reproductive success does not appear to be important, however.

We will use seven cohorts of marked penguins from each colony to assess juvenile survival, recruitment age, and age-specific fecundity and subsequent survival. These data will be compared with another demographic study, the only one for this species, conducted at Cape Crozier during the 1960s and 1970s when populations were declining.

Information will be related to sea ice as quantified by satellite images. Global climate is changing fastest in the polar regions. The Adélie penguin is tied to sea ice, a primary factor in rapid polar climate change (less sea ice, less reflection of solar energy). The extreme sensitivity of these penguins to climate change has been often noted. Understanding the demographic mechanisms behind this sensitivity will contribute greatly to knowledge of the effects of climate change on antarctic marine organisms. (BO-031-O; NSF/OPP 01-25608)

Investigations of abandoned penguin colonies in Antarctica.

Steven Emslie, University of North Carolina.

Climate change is assumed to be a pivotal factor in the success of many species. This project will investigate the history of Adélie penguins in late Holocene Antarctica. By locating and examining the fossil remains of former colonies, scientists hope to develop a model of when they thrived and when colonies were abandoned-and thus their success-relative to climate change. This model could inform current science on the relationship between climate and population dynamics.

Our study will integrate data from the ecological, geological, and paleobiological records with satellite-imagery analyses. The climate factor will be inferred by data contemporaneous with the fossil evidence, in particular the extent of the sea ice and marine productivity. The population factor will be developed through field and laboratory investigations of abandoned colonies along coastal Antarctica.

Researchers will first collect surface and subsurface bones, feathers, and eggshell fragments preserved at these sites; later, in the laboratory, scientists can reconstruct the occupation history of each abandoned colony through standard and radiocarbon analyses. Sediments from each site will be sifted to recover organic remains (such as squid beaks and fish otoliths) believed to be the staples of the penguin diet. Statistical analysis of such indicators can trace the changing size of the colony at specific prehistoric times, and thus consumption of prey becomes a proxy for population success. This timeline can then be matched to past episodes of climate change, which are well documented for the late Pleistocene and Holocene in ice-core and marine sediment records.

We expect these ancient responses by penguins to climate change (as indicated by the paleoecological record) to parallel those observed in Antarctica today, where regional warming has been documented over the past 20 to 50 years. Ultimately, we will be able to test the hypothesis that Adélie penguins have been responding to climate change in a predictable manner for decades and centuries and that those responses can be anticipated, relative to fluctuations in the extent of sea ice and marine productivity. (BO-034-O; NSF/OPP 99-09274)

Cold temperature as an evolutionary shaping force in the physiology of the antarctic fishes.

Bruce D. Sidell, University of Maine.

Notothenioid fishes have been evolving for 10 to 14 million years at a nearly constant body temperature of $\sim 0^{\circ}\text{C}$. Many unusual characteristics of these fishes are adaptations to life at cold body temperatures or physiological or biochemical features permitted by life at cold body temperatures but otherwise deleterious. Our three major objectives will entail a combination of shipboard collection of fishes and experimentation at Palmer Station, with more extensive and sophisticated laboratory analyses on samples in the United States.

Our first aim is to identify the amino acid substitutions in the fatty acid-binding pocket of fatty acyl coenzyme A synthetase (FACS) from antarctic fishes. Fatty acids are a major source of energy in these fishes, and FACS is essential to their metabolism. Site-directed mutagenesis will be used to produce modified antarctic fish FACS in which specific amino acids have been mutated to those of consensus sequences from warmer-bodied vertebrate animals. These experiments may permit us to determine the specific substitutions that explain both substrate specificity and preservation of catalytic rate of notothenioid FACS at cold temperatures.

Our second goal is to produce a rigorous biochemical and biophysical characterization of an intracellular binding protein, parvalbumin, from antarctic fishes. Parvalbumin plays a pivotal role in facilitating the relaxation of fast-contracting muscles and is a likely site of strong selective pressure. Preliminary data strongly indicate that in antarctic fishes, the protein has been modified to function at cold temperatures. Full-length clones for antarctic fish parvalbumin(s) will be obtained. In combination with already available information, these data will yield insight into their functioning at very cold body temperatures.

Our third goal is to conduct a broad survey of the pattern of cardiac myoglobin (Mb) expression in the Notothenioidei. Previous work has indicated a variable pattern of presence or absence of Mb in the hearts of icefishes, probably due to the unusually low niche competition in the Southern Ocean. It is likely that similar loss of cardiac Mb will be observed in other notothenioid taxa. We will survey as many notothenioid species as possible and will use molecular biological techniques to determine the mechanism(s) responsible for loss of Mb

expression. (BO-036-O; NSF/OPP 01-25890)

Structure, function, and expression of tubulins, globins, and microtubule-dependent motors from cold-adapted antarctic fishes.

H. William Detrich III, Northeastern University.

As the Southern Ocean cooled during the past 25 million years, the fishes of antarctic coastal waters evolved biochemical and physiological adaptations that maintain their essential cellular processes. The long-range goals of our research are to determine, at the molecular level, the adaptations that enhance the assembly of microtubules (thin tubes made of protein and used to make structures involved in cellular movement), the function of kinesin motors, and the expression of globin and tubulin genes. Our specific objectives are

- to determine the primary sequence changes and posttranslational modifications that contribute to the efficient polymerization of antarctic fish tubulins (globular proteins) at low temperatures;
- to determine the primary sequence changes and posttranslational modifications that contribute to the efficient polymerization of antarctic fish tubulins (globular proteins) at low temperatures;
- to characterize the structure, organization, and promoter-driven expression of globin and tubulin genes from an antarctic rockcod (*Notothenia coriiceps*) and a temperate congener (*N. angustata*).

Brain tubulins from antarctic fishes differ from those of temperate and warm-blooded vertebrates both in unusual primary sequence substitutions and in posttranslational C-terminal glutamylation. Potential adaptations of antarctic fish tubulins will be tested directly by production of wild-type and site-directed tubulin mutants for functional laboratory analysis. We will determine the capacity of fish tubulins to form "cold-stable" microtubules, and we will test the role of the carboxy-terminal charge status of tubulin in cold adaptation of microtubule assembly after enzymatic manipulation.

Three unusual substitutions in the kinesin motor domain of *Chionodraco rastrospinosus* may enhance mechanochemical activity at low temperatures. To test the functional significance of these changes, fish residues will be converted to those found in mammalian brain kinesin. Reciprocal substitutions will be introduced into the framework of the mammalian kinesin motor domain. After production in *Escherichia coli* and purification, the functional performance of the mutant motor domains will be evaluated.

Also, molecular adaptation of gene expression in *N. coriiceps* will be analyzed. Structural features that support efficient expression will be assessed. Comparison with *N. angustata* should help delineate elements of the regions that are important for high-level expression at low temperatures. The functions of possible regulatory elements will be tested by deletion analysis and by specific mutagenesis. Together, these studies should reveal the molecular adaptations of antarctic fishes that maintain efficient cytoskeletal assembly, mechanochemical motor function, and gene expression at low temperatures and advance the molecular understanding of the poikilothermic mode of life. (BO-037-L; NSF/OPP 00-89451)

Investigations on deterioration in the historic huts of the Ross Sea region of Antarctica.

Robert A. Blanchette, University of Minnesota.

During the first two decades of the 20th century-Antarctica's "Heroic Era"-Europeans mounted a handful of expeditions in hopes of reaching (and claiming) the geographical South Pole. Base camps established in the McMurdo Sound region by Scott at Cape Evans and Shackleton at Cape Royds were abandoned once the expeditions were over, leaving behind thousands of artifacts, as well as the huts the explorers built for shelter and storage. Over the intervening 90 years, the extremes of the polar environment have actually protected some of the artifacts from rapid decay, but conservators have recently become concerned about serious degradation of

what is an important historical, archaeological site.

Some of the most exigent threats are as follows:

- Wood in contact with the ground is being destroyed by a specific wood-destroying fungus. Various molds and cellulose-degrading fungi are attacking artifacts made of leather, textiles, and other organic materials.
- Exterior wood is being degraded by nonbiological processes of deterioration as well, including salt, ultraviolet radiation, and wind erosion.
- Chemical damage within the huts is apparent, and the soils on the site are contaminated with aromatic hydrocarbons from petroleum products.

We plan to identify the biological and nonbiological agents responsible for the deterioration, study the mechanisms and progressive sequence of events taking place during the decay processes, test methods to be used to control future deterioration, determine the extent of environmental pollutants in soils at the historic sites, and evaluate chemical spills within the huts. The goal is to provide the scientific data conservators need to help protect these important historic sites for future generations. But the project should also shed light on these unique deterioration processes, as well as augment scientific understanding of the biology of antarctic microorganisms and the biodiversity of microbes present in this unusual environment. (BO-038-O; NSF/OPP 99-09271)

Penguin-krill-ice interactions: The impact of environmental variability on penguin demography.

Wayne Trivelpiece, Southwest Fisheries Science Center, National Oceanic and Atmospheric Administration.

How well organisms thrive in their environment is often revealed by basic ecological relationships. For two decades, data have been collected on several species of penguins, including the Adélie, gentoo, and chinstrap, at Admiralty Bay on King George Island in the Antarctic Peninsula. Looking at some of the basic aspects of the lives of these predators, such as survival and recruitment, population size and breeding success, and diets and foraging ecology, scientists have been able to develop and test key hypotheses about variability in the antarctic marine ecosystem.

To explore these relationships, we will periodically capture adult and juvenile penguins to band, measure, and weigh them, and to collect blood and diet samples for genetic and physiologic studies. During the breeding season, the penguins and the sea ice will be observed by satellite. Another aspect of the population biology of penguins relates to the possible impact of commercial fishing, so this study will provide useful information to the Convention for the Conservation of Antarctic Marine Living Resources, which is the part of the Antarctic Treaty System that focuses on fisheries management. (BO-040-E; NSF/OPP 99-80641)

Seasonal dynamics of giant agglutinated foraminifera.

Samuel Bowser, New York State Department of Health.

Found in all marine environments, foraminifera ("forams") are single-celled, shelled (agglutinated) creatures with a key role in the ocean food web. They may be planktonic (floating in the water) or benthic (living on shells, rock, or seaweed, or in the sand or mud at the bottom of the ocean). Their characteristic habitats and the chemistry of their shells (which reflects the qualities of the local water they live in) make them very useful to scientists as an indicator of when and under what conditions they lived. Antarctica and the Southern Ocean ecology are no exception.

Previous studies have shown that the forams in Explorers Cove in McMurdo Sound consume a wide variety of

prey, ranging from bacteria through a taxonomically diverse group of metazoans, including juvenile invertebrates. These studies have been restricted to specimens collected from October through early December, immediately following the austral winter.

But in the succeeding months of the austral summer, a burst of biological productivity occurs, both under the ice and in the benthos. Lacking studies of this period, we do not know how the forams might be responding to this summer food pulse. Looking at such indices as species composition, densities, size distribution, and others, we plan to document changes in relevant abiotic and biotic factors in the Explorers Cove benthos from austral spring to late summer and to characterize how the agglutinated foram community structure responds. To accomplish these analyses, we will use sediment cores, underwater microscopy, molecular tools, isotope analysis of lipids, and some other newly refined methods.

We expect these combined approaches to elucidate the roles played by larger agglutinated forams in the Explorers Cove benthic food web, especially the ways these roles may change consequent to the summer food pulse. Further, the results of these studies should have wider significance in the ocean sciences because Explorers Cove and its agglutinated foram assemblage are comparable to many bathyal and abyssal deep-sea localities.

To enhance insight into marine processes associated with global climate change, we are also collaborating with investigators from Russia to

- test the universality of meltwater turbidity impacts documented in the Arctic,
- assess changes (by adapting modern biochemical and molecular assays) in the living foraminiferal assemblage in response to glacial meltwater, and
- explore ways of revealing the imprint of glacial proximity in the antarctic fossil record. (BO-043-O; NSF/OPP 00-03639)

Interannual variability in the antarctic Ross Sea (IVARS): Nutrients and season production.

Walker Smith, Virginia Institute of Marine Sciences.

During the past few decades, oceanographers and other scientists have found significant variations in Southern Ocean biogeochemical processes from year to year. Some of the more significant of these interannual variations are the ice extent and concentration, the composition of herbivore communities, and the distributions and reproductive success of bird and marine mammals.

Surprisingly-because it is so central to the food web-little is known about how phytoplankton production varies from year to year or what role these variations may play. The production system in the Ross Sea consists predominantly of two major functional groups: diatoms and *Phaeocystis antarctica*, a colonial haptophyte. In this project, we will collect time-series data and assess the interannual variations of phytoplankton in the southern Ross Sea, Antarctica.

The Ross Sea provides a unique setting for such an investigation. We can build on a de facto, already ongoing time-series because so many studies have been conducted in the Ross Sea in the past decade. Also, it has been established that there are fewer species there (relative to some other sites) and that seasonal production is as great as anywhere in the Antarctic. Most important, seasonal production of the total phytoplankton community (as well as its two functional groups) can be estimated from late summer nutrient profiles.

Interannual variations in seasonal production (and of the two major taxa of producers) may be an important factor in the growth and survival of higher trophic levels within the Ross Sea food web. They also shed light on

the natural variability of the suite of biogeochemical processes in the region. Having a scientific handle on that baseline of change is important, because of the scientific efforts to model how climate may change in the future. As climate changes, so certainly will biology be profoundly affected, and to model and evaluate such change we need to place it in the context of natural interannual variability. (BO-047-O; NSF/OPP 00-87401)

Evolutionary loss of the heat-shock response in antarctic fishes.

Gretchen Hofmann, Arizona State University-Tempe.

Evolution has crafted a way for organisms to respond to the stress of abrupt environmental changes, in particular a sudden elevation of temperature. Commonly viewed as a universal characteristic of organisms, the heat-shock response (HSR) triggers previously inactive genes to synthesize one or more classes of molecular chaperones, known as heat-shock proteins (Hsps). But what about Antarctica, where such a sudden burst of heat is so unlikely? In previous studies on a cold-adapted, stenothermal antarctic teleost fish, *Trematomus bernacchii*, it was determined that this adaptational response has been lost over evolutionary time.

If evolution at subzero temperatures has indeed altered the gene expression patterns for molecular chaperones in antarctic fish, then the study of how cells respond to temperature at a molecular level may be a legitimate new frontier in biology. At this stage, however, though HSR-perhaps the quintessential example of the environmental regulation of gene expression-has been well described at the cellular level, there is little information on how the response is actually regulated in ectothermic animals in a natural environment.

We hope to build on that evolutionarily significant observation by examining this profound change in the environmental regulation of gene expression on two levels. First, we will try to establish how widespread the loss of the HSR might be in the suborder Notothenioidei, including antarctic and nonantarctic members of the group. Second, we will try to determine the nature of the lesion in gene expression that accounts for the loss of the expression of stress-inducible genes in antarctic species. Both of these objectives will entail experiments on closely related, cold temperate species from New Zealand waters.

Ultimately, the lesions in the Hsp gene expression in antarctic notothenioids may serve to highlight aspects of the "cellular thermostat" and to provide key information about the actual molecular response mechanism triggered by environmental stress. The results should contribute to our knowledge of the environmental physiology and evolutionary biology of the antarctic notothenioid fishes, as well as enhance our understanding of the extreme stenothermality in these fish. (BO-134-O; NSF/OPP 00-87971)

Gene expression in extreme environments: Extending microarray technology to understand life at its limits.

Alison Murray, Desert Research Institute.

One of the most difficult challenges facing scientists who study life in extreme environments is observing the organisms in situ and then extrapolating those observations into descriptions that capture both the unique aspects of life and the adaptations required for survival. Antarctic marine psychrophiles (cold-loving organisms) provide an excellent model group of extreme microorganisms to study; since very little is known about their biological and functional diversity or about the metabolic adaptations they have developed to live at -1.8°C.

This project is centered not only on identifying the organisms present in antarctic marine waters, but it also entails a significant effort in technology development of DNA microarrays for use with environmental samples. Our approach includes sequencing DNA cloned directly from the environment, then querying the identified open reading frames by hybridization to freshly expressed mRNA. We hope to determine relative levels of gene expression for a suite of genes from bacterial and archaeal genomes with functions essential for cellular growth, as well as functions related to cold tolerance and membrane adaptation.

This effort to develop functional genomics approaches for the study of microorganisms in situ may well have

fairly direct practical benefits. High-throughput screening of putative psychrophilic genes isolated from extreme environments may identify new genes for use in biotechnology. By discovering these genes in natural (extreme) environments, we can learn about gene function and develop hypotheses on potential metabolic roles, without the requirement of microbial cultivation.

The details of this work entail

- sequencing six large bacterial genomic DNA fragments isolated directly from antarctic marine psychrophiles,
- constructing two different types of DNA microarrays designed to identify genes being actively expressed in uncultivated microorganisms (archaea and bacteria) living in the subzero marine waters of the Antarctic,
- optimizing specific aspects of microarray technology for use with environmental samples, and
- developing a transferable methodology that will be useful for other researchers in accessing information on gene expression directly from the natural environment. (BO-179-O; NSF/OPP 00-85435)

Effects of the iceberg B-15 on the breeding success of the Cape Crozier emperor penguin colony.

Gerald Kooyman, Scripps Institution of Oceanography, University of California-San Diego.

This project will investigate the effects of the iceberg, B-15, on the emperor penguin (*Aptenodytes fosteri*) population at Cape Crozier. The population of this southernmost of the emperor penguin colonies, although sometimes fluctuating radically, had grown steadily in past years, with as many as 1,200 chicks counted. This probably represented an adult population of 2,400 to 3,000 birds. However, in 2001, after B-15 ground into the Cape Crozier area during the winter breeding period, no live emperor chicks were found. The colony had disappeared.

The goal of this project is to determine whether the colony will re-establish itself at Cape Crozier or relocate to a different site nearby. If the colony re-establishes at Cape Crozier, we will estimate the previous year's loss with a census of the chicks present this year. The destruction of the colony site by the iceberg in 2001 represents a natural experiment to examine the resilience of breeding emperor penguins to short-term disasters. Broader impacts of this study are related to the historical importance and worldwide interest in this colony, since it was the first emperor penguin colony discovered and has probably the longest census record of any penguin colony. (BO-197-O; NSF/OPP 02-24957)

Monitoring the effects of tourism and environmental variability on Adélie penguins at Palmer Station, Antarctica.

William R. Fraser, Polar Oceans Research Group.

The potential consequences of antarctic tourism on Adélie penguins (*Pygoscelis adeliae*) have been debated for more than 20 years. However, the rapid proliferation of these activities since 1970, particularly on the Antarctic Peninsula, has not only forced an extension of these questions to wildlife populations in general, but also colored them with a sense of urgency and controversy that has polarized opinions. The key concern is that continued increases in these activities will eventually overcome the ability of research to address critical issues in a timely and biologically meaningful manner. This is a valid concern, since studies to examine human impacts have either not been implemented at critical sites or are limited in scope because of logistic and experimental constraints.

Understanding how tourism might affect Adélie penguins rests fundamentally on the need to quantify and understand the natural variability manifested by breeding populations over spatial and temporal scales. However,

although it is generally recognized that without these data it will be difficult to critically assess any localized changes from tourism, this ecosystem approach is expensive and complex and is not likely to be justified by the need to understand tourist impacts.

We will continue a tourist monitoring program underway at Palmer Station as part of a large ecosystem-scale study. Palmer Station mirrors current patterns in tourism and tourist-wildlife interactions in the western Antarctic Peninsula. It also provides unique opportunities for research on human impacts. This includes the presence of long-term databases that document environmental variability over time and space scales in both marine and terrestrial habitats, as well as the ability to examine potential tourist impacts as part of controlled experiments.

This research is expected to capitalize and expand on two key findings to date. One is the discovery of a previously unrecognized source of variability in the Adélie penguin population that results from interactions between landscape geomorphology and changing patterns of snow deposition due to climate warming. The other is the observation that penguins breeding in less desirable landscapes may be more susceptible to cumulative impacts induced by the presence of human activity.

These findings have important implications for understanding interactions between climate change and ecosystem response, and for detecting, mitigating, and managing the consequences of human activities such as tourism. (BO-198-P; NSF/OPP 01-30525)

Effects of foraging on the lipid biochemistry of freely diving Weddell seals (*Leptonychotes weddellii*).

Michael Castellini, University of Alaska-Fairbanks, and Lorrie Rea, University of Central Florida.

Freely diving Weddell seals in Antarctica offer a unique opportunity to follow the biochemistry and physiology of nutrient use in a large carnivore.

A study of the in vivo nutritional biochemistry of foraging in a free-ranging, large mammalian carnivore has never been attempted because of the logistics of obtaining multiple blood samples, conducting turnover studies, and measuring digestive chemistry while the animal is actively foraging. Although such studies can be conducted in laboratory or zoo settings, they are limited to using captive animals whose feeding times and diets are typically constrained by humans.

A unique opportunity exists in the Antarctic. For several decades, the Weddell seal has been the focus of natural diving physiology studies using isolated holes through the sea ice near McMurdo Station. The seal has access to a single ice hole where it routinely returns to breathe, sleep, digest, and so on. With the use of blood-sampling catheters, we have been able to collect serial samples whenever the seal returns to the surface between dives. During such experiments, these seals actively catch and digest their prey. However, all previous studies have focused on diving physiology per se because they were designed to examine how the animals tolerated long periods of holding their breath. Any observations on nutritional chemistry were incidental and not part of the study design.

We propose to take this method in a new direction by examining how Weddell seals process nutrients while foraging. Like all seals, Weddell seals rely primarily on lipid metabolism for daily energy. Therefore, we will examine the kinetics of lipid uptake and use during active foraging bouts. We will obtain blood samples from freely diving animals and use labeled traced experiments to quantify lipid turnover rates and separate the lipid pool into its various components. We also will compare lipid uptake and use in adult seals and in pups, which are biochemically adapted for massive and rapid lipid use while nursing.

This project will provide important insights into mammalian biochemistry. These data will be important not only to antarctic ecosystem studies, but also to the entire field of lipid metabolism in mammals and the study of carnivore biology. (BO-199-O; NSF/OPP 01-30417)

Latitudinal effects of ultraviolet radiation on bacterioplankton: BRIDE OF TABASCO science of opportunity cruise.

Wade H. Jeffrey, University of West Florida.

Our objectives are to examine changes in response to ultraviolet radiation along the latitudinal transect between Punta Arenas and San Diego. Ultra-violet irradiance intensity will change by almost an order of magnitude along the transect. We will conduct daily experiments with surface waters collected at dawn to

- examine changes in the response of bacterioplankton and phytoplankton to changes in incident irradiance using radioisotope incorporation assays;
- study levels of ultraviolet-induced DNA damage under changing incident irradiance;
- evaluate the role of nutrients, particularly iron, in determining microbial response to ultraviolet radiation;
- field-test an iron bioreporter system; and
- examine changes in bacterial community structure and function in response to ultraviolet radiation. (BO-200)

Viral dynamics and the Southern Ocean iron-cycle.

Steven Wilhelm, University of Tennessee-Knoxville.

The bioavailability of iron has been shown to regulate primary production in high-nutrient low-chlorophyll (HNLC) marine environments such as are found in Antarctica. More than 99 percent of dissolved iron in HNLC systems is organically complexed, and these iron-ligand complexes represent (at least indirectly) the pool of iron that is available to marine plankton. However, the character and source of the iron-binding ligands in sea water are unknown.

Recent research has suggested that the activity of naturally occurring viral populations provides enough organically complexed iron to regenerate the concentrations of dissolved iron measured in an HNLC coastal upwelling system in a time frame consistent with the growth of the phytoplankton community. Our goal is to participate in the upcoming (January-February 2003) *FeCycle* analysis and, in collaboration with scientists from the University of Otago (New Zealand) and the University of Delaware, to determine the rate at which viruses recycle iron back to the marine microbial community.

A 12-day experiment in the vicinity of 46° 30' S, 178° 30' E will build on 4 years of research in this region. The overall objective of the project is to collect information that will allow us to develop a preliminary model for the cycling of iron in this system in the absence of iron fertilization. (BO-229-O; NSF/OPP 02-28895)

Prevention of environment-induced decrements in mood and cognitive performance.

Laurence A. Palinkas, University of California-San Diego.

Cognitive performance degrades with residence in Antarctica, and mood alteration fits a seasonal pattern during extended residence. Although these changes suggest psychological responses to physiological adaptations to cold and dim light, the exact mechanisms are poorly understood.

Our first objective is to determine whether long-term exposure to cold temperatures and/or to dim light is associated with significant changes in cognitive performance and emotional well-being:

- Is physiological adaptation to cold and/or adaptation to dim light independently or synergistically associated with decrements in cognitive performance and emotional well-being?
- Do personnel at South Pole Station experience greater physiological adaptation and decrements than personnel at McMurdo Station?

We also wish to determine whether these decrements can be prevented or minimized by pharmacologic interventions and/or phototherapy:

- What are the effects of combining liothyronine sodium with levothyroxine sodium versus supplementation with tyrosine (a precursor to both thyroid hormone and catecholamines) and daily phototherapy?
- Is phototherapy used in combination with a pharmacologic agent more effective than either intervention used alone.

In phase I, we will establish computer-testing protocols, develop an effective placebo capsule, package the necessary drugs, and test the validity and reliability of computer-administered cognition and mood protocols with 30 hypothyroid outpatients on constant thyroid hormone replacement and 30 age- and sex-matched healthy controls in New Zealand.

In phase II, 50 members of the 2002 winter crews, 35 at McMurdo Station and 15 at South Pole Station, will be randomized in a double-blind crossover design into 1 of 2 treatment groups (20 subjects in each group) and 1 control group (10 subjects). Baseline measurements will be conducted, and treatment groups will be switched after a 1-month washout period. Mood and memory testing will comprise 5 assessments over 12 months. Treatments consist of 50 micrograms (mcg) of levothyroxine sodium plus 12.5 mcg of liothyronine per day, 150 milligrams per kilogram of tyrosine per day, and a placebo.

In phase III, a similar design will be used to evaluate the effectiveness of phototherapy, alone and in combination with the more effective of the two pharmacologic interventions.

Our research will lead to an improved understanding of the specific environmental conditions and physiological mechanisms that affect behavior and performance in the Antarctic, help develop countermeasures for circannual oscillations of mood and cognitive performance, and contribute to a reduction in accidental injuries at high latitudes. (BO-321-M/S; NSF/OPP 00-90343)

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